

Att. #10

SEQUENCE LISTING

NE (1) GENERAL INFORMATION:

- (i) APPLICANT: Lee, Jong Y.
- (ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C., P.A.
 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/016,159
 - (B) FILING DATE: 30-JAN-1998
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/876,227
 - (B) FILING DATE: 16-JUN-1997
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/734,097
 - (B) FILING DATE: 21-OCT-1996
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/460,525
 - (B) FILING DATE: 02-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ellinger, Mark S.
 - (B) REGISTRATION NUMBER: 34,812
 - (C) REFERENCE/DOCKET NUMBER: 07004/002004
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612/335-5070
 - (B) TELEFAX: 612/288-9696

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: BamHI linker at 5' end followed by sequence for amino acids 25 through 29 of the full length human Epor protein. Forward primer for Sequence ID No. 2."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGATCC GCG CCC CCG CCT A AC
Ala Pro Pro Pro
1

23

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: EcoRI linker followed by sequence complementary to coding sequence for amino acids 226 through 222 of full length human Epor protein. Reverse primer for Sequence ID No. 1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAATTCCGGG GTCCAGGTCG CT

22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)

(ix) FEATURE:

(A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Smith, D.B.

Johnson, K.S.

(B) TITLE: Single-step purification of polypeptides
expressed in Escherichia coli as fusions with
glutathione-S-transferase

(D) VOLUME: 67

(F) PAGES: 31-40

(G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTG GTT CCG CGT GGA T CC

Leu Val Pro Arg Gly

5

18

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1527 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Winkelmann, J. C., et al.

(C) JOURNAL: Blood

(D) VOLUME: 76

(E) ISSUE: 1

(F) PAGES: 24-30

(G) DATE: 1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT	48
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys	
1 5 10 15	
CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC	96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp	
20 25 30	
CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA	144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu	
35 40 45	
GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG	192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp	
50 55 60	
GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC	240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser	
65 70 75 80	
TAC CAG CTC GAG GAT GAG CCA TGG AAG CTG TGT CGC CTG CAC CAG GCT	288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala	
85 90 95	

CCC	ACG	GCT	CGT	GGT	CGG	GTG	CGC	TTC	TGG	TGT	TCG	CTG	CCT	ACA	GCC	336
Pro	Thr	Ala	Arg	Gly	Arg	Val	Arg	Phe	Trp	Cys	Ser	Leu	Pro	Thr	Ala	
			100					105					110			
GAC	ACG	TCG	AGC	TTC	GTG	CCC	CTA	GAG	TTG	CGC	GTC	ACA	GCA	GCC	TCC	384
Asp	Thr	Ser	Ser	Phe	Val	Pro	Leu	Glu	Leu	Arg	Val	Thr	Ala	Ala	Ser	
		115					120					125				
GGC	GCT	CCG	CGA	TAT	CAC	CGT	GTC	ATC	CAC	ATC	AAT	GAA	GTA	GTG	CTC	432
Gly	Ala	Pro	Arg	Tyr	His	Arg	Val	Ile	His	Ile	Asn	Glu	Val	Val	Leu	
	130					135					140					
CTA	GAC	GCC	CCC	GTG	GGG	CTG	GTG	GCG	CGG	TTG	GCT	GAC	GAG	AGC	GGC	480
Leu	Asp	Ala	Pro	Val	Gly	Leu	Val	Ala	Arg	Leu	Ala	Asp	Glu	Ser	Gly	
145					150					155					160	
CAC	GTA	GTG	TTG	CGC	TGG	CTC	CCG	CCG	CCT	GAG	ACA	CCC	ATG	ACG	TCT	528
His	Val	Val	Leu	Arg	Trp	Leu	Pro	Pro	Pro	Glu	Thr	Pro	Met	Thr	Ser	
				165					170					175		
CAC	ATC	CGC	TAC	GAG	GTG	GAC	GTC	TCG	GCC	GGC	AAC	CGG	CCA	GGG	AGC	576
His	Ile	Arg	Tyr	Glu	Val	Asp	Val	Ser	Ala	Gly	Asn	Arg	Pro	Gly	Ser	
			180					185					190			
GTA	CAG	AGG	GTG	GAG	ATC	CTG	GAG	GGC	CGC	ACC	GAG	TGT	GTG	CTG	AGC	624
Val	Gln	Arg	Val	Glu	Ile	Leu	Glu	Gly	Arg	Thr	Glu	Cys	Val	Leu	Ser	
		195					200					205				
AAC	CTG	CGG	GGC	CGG	ACG	CGC	TAC	ACC	TTC	GCC	GTC	CGC	GCG	CGT	ATG	672
Asn	Leu	Arg	Gly	Arg	Thr	Arg	Tyr	Thr	Phe	Ala	Val	Arg	Ala	Arg	Met	
	210					215					220					
GCT	GAG	CCG	AGC	TTC	GGC	GGC	TTC	TGG	AGC	GCC	TGG	TCG	GAG	CCT	GTG	720
Ala	Glu	Pro	Ser	Phe	Gly	Gly	Phe	Trp	Ser	Ala	Trp	Ser	Glu	Pro	Val	
225					230					235					240	
TCG	CTG	CTG	GAG	CCT	AGC	GAC	CTG	GAC	CCC	CTC	ATC	CTG	ACG	CTC	TCC	768
Ser	Leu	Leu	Glu	Pro	Ser	Asp	Leu	Asp	Pro	Leu	Ile	Leu	Thr	Leu	Ser	
				245					250					255		
CTC	ATC	CTC	GTG	GTC	ATC	CTG	GTG	CTG	CTG	ACC	GTG	CTC	GCG	CTG	CTC	816
Leu	Ile	Leu	Val	Val	Ile	Leu	Val	Leu	Leu	Thr	Val	Leu	Ala	Leu	Leu	
			260					265					270			
TCC	CAC	CGC	CGG	GCT	CTG	AAG	CAG	AAG	ATC	TGG	CCT	GGC	ATC	CCG	AGC	864
Ser	His	Arg	Arg	Ala	Leu	Lys	Gln	Lys	Ile	Trp	Pro	Gly	Ile	Pro	Ser	
		275					280					285				
CCA	GAG	AGC	GAG	TTT	GAA	GGC	CTC	TTC	ACC	ACC	CAC	AAG	GGT	AAC	TTC	912
Pro	Glu	Ser	Glu	Phe	Glu	Gly	Leu	Phe	Thr	Thr	His	Lys	Gly	Asn	Phe	
	290					295					300					
CAG	CTG	TGG	CTG	TAC	CAG	AAT	GAT	GGC	TGC	CTG	TGG	TGG	AGC	CCC	TGC	960
Gln	Leu	Trp	Leu	Tyr	Gln	Asn	Asp	Gly	Cys	Leu	Trp	Trp	Ser	Pro	Cys	
305					310					315					320	
ACC	CCC	TTC	ACG	GAG	GAC	CCA	CCT	GCT	TCC	CTG	GAA	GTC	CTC	TCA	GAG	1008
Thr	Pro	Phe	Thr	Glu	Asp	Pro	Pro	Ala	Ser	Leu	Glu	Val	Leu	Ser	Glu	
				325					330					335		
CGC	TGC	TGG	GGG	ACG	ATG	CAG	GCA	GTG	GAG	CCG	GGG	ACA	GAT	GAT	GAG	1056
Arg	Cys	Trp	Gly	Thr	Met	Gln	Ala	Val	Glu	Pro	Gly	Thr	Asp	Asp	Glu	

340										345					350					
GGC	CCC	CTG	CTG	GAG	CCA	GTG	GGC	AGT	GAG	CAT	GCC	CAG	GAT	ACC	TAT	1104				
Gly	Pro	Leu	Leu	Glu	Pro	Val	Gly	Ser	Glu	His	Ala	Gln	Asp	Thr	Tyr					
		355				360				365										
CTG	GTG	CTG	GAC	AAA	TGG	TTG	CTG	CCC	CGG	AAC	CCG	CCC	AGT	GAG	GAC	1152				
Leu	Val	Leu	Asp	Lys	Trp	Leu	Leu	Pro	Arg	Asn	Pro	Pro	Ser	Glu	Asp					
		370				375				380										
CTC	CCA	GGG	CCT	GGT	GGC	AGT	GTG	GAC	ATA	GTG	GCC	ATG	GAT	GAA	GGC	1200				
Leu	Pro	Gly	Pro	Gly	Gly	Ser	Val	Asp	Ile	Val	Ala	Met	Asp	Glu	Gly					
		385				390				395		400								
TCA	GAA	GCA	TCC	TCC	TGC	TCA	TCT	GCT	TTG	GCC	TCG	AAG	CCC	AGC	CCA	1248				
Ser	Glu	Ala	Ser	Ser	Cys	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Pro	Ser	Pro					
				405				410				415								
GAG	GGA	GCC	TCT	GCT	GCC	AGC	TTT	GAG	TAC	ACT	ATC	CTG	GAC	CCC	AGC	1296				
Glu	Gly	Ala	Ser	Ala	Ala	Ser	Phe	Glu	Tyr	Thr	Ile	Leu	Asp	Pro	Ser					
		420				425						430								
TCC	CAG	CTC	TTG	CGT	CCA	TGG	ACA	CTG	TGC	CCT	GAG	CTG	CCC	CCT	ACC	1344				
Ser	Gln	Leu	Leu	Arg	Pro	Trp	Thr	Leu	Cys	Pro	Glu	Leu	Pro	Pro	Thr					
		435				440				445										
CCA	CCC	CAC	CTA	AAG	TAC	CTG	TAC	CTT	GTG	GTA	TCT	GAC	TCT	GGC	ATC	1392				
Pro	Pro	His	Leu	Lys	Tyr	Leu	Tyr	Leu	Val	Val	Ser	Asp	Ser	Gly	Ile					
		450				455				460										
TCA	ACT	GAC	TAC	AGC	TCA	GGG	GAC	TCC	CAG	GGA	GCC	CAA	GGG	GGC	TTA	1440				
Ser	Thr	Asp	Tyr	Ser	Ser	Gly	Asp	Ser	Gln	Gly	Ala	Gln	Gly	Gly	Leu					
		465				470				475				480						
TCC	GAT	GGG	CCC	TAC	TCC	AAC	CCT	TAT	GAG	AAC	AGC	CTT	ATC	CCA	GCC	1488				
Ser	Asp	Gly	Pro	Tyr	Ser	Asn	Pro	Tyr	Glu	Asn	Ser	Leu	Ile	Pro	Ala					
		485				490						495								
GCT	GAG	CCT	CTG	CCC	CCC	AGC	TAT	GTG	GCT	TGC	TCT	TAG				1527				
Ala	Glu	Pro	Leu	Pro	Pro	Ser	Tyr	Val	Ala	Cys	Ser									
		500				505														

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asp	His	Leu	Gly	Ala	Ser	Leu	Trp	Pro	Gln	Val	Gly	Ser	Leu	Cys
1				5					10					15	
Leu	Leu	Leu	Ala	Gly	Ala	Ala	Trp	Ala	Pro	Pro	Pro	Asn	Leu	Pro	Asp
			20					25					30		
Pro	Lys	Phe	Glu	Ser	Lys	Ala	Ala	Leu	Leu	Ala	Ala	Arg	Gly	Pro	Glu
		35					40					45			

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
 50 55 60
 Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
 65 70 75 80
 Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
 85 90 95
 Pro Thr Ala Arg Gly Arg Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
 100 105 110
 Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
 115 120 125
 Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
 130 135 140
 Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
 145 150 155 160
 His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
 165 170 175
 His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Arg Pro Gly Ser
 180 185 190
 Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
 195 200 205
 Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
 210 215 220
 Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
 225 230 235 240
 Ser Leu Leu Glu Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
 245 250 255
 Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
 260 265 270
 Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
 275 280 285
 Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
 290 295 300
 Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys
 305 310 315 320
 Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu
 325 330 335
 Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu
 340 345 350
 Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr
 355 360 365
 Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp
 370 375 380

Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly
 385 390 395 400
 Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro
 405 410 415
 Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser
 420 425 430
 Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr
 435 440 445
 Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile
 450 455 460
 Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu
 465 470 475 480
 Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala
 485 490 495
 Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser
 500 505